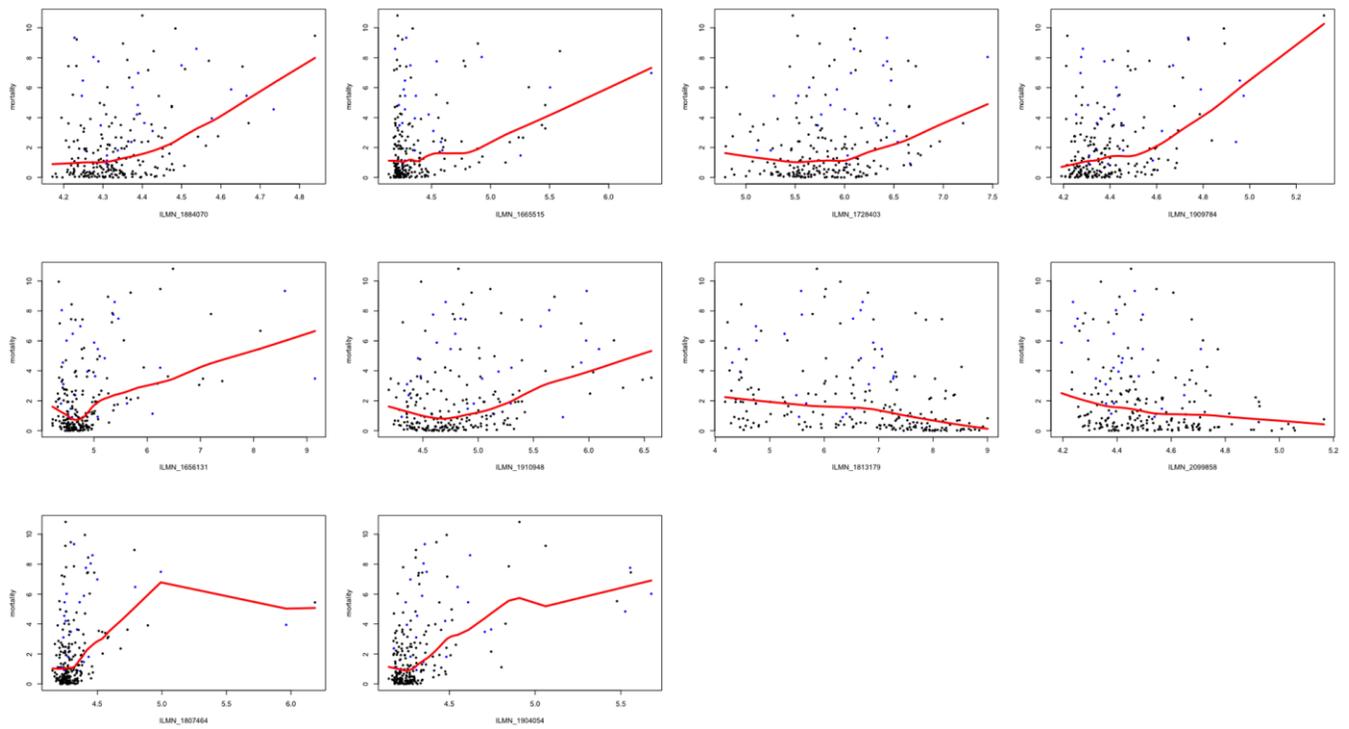
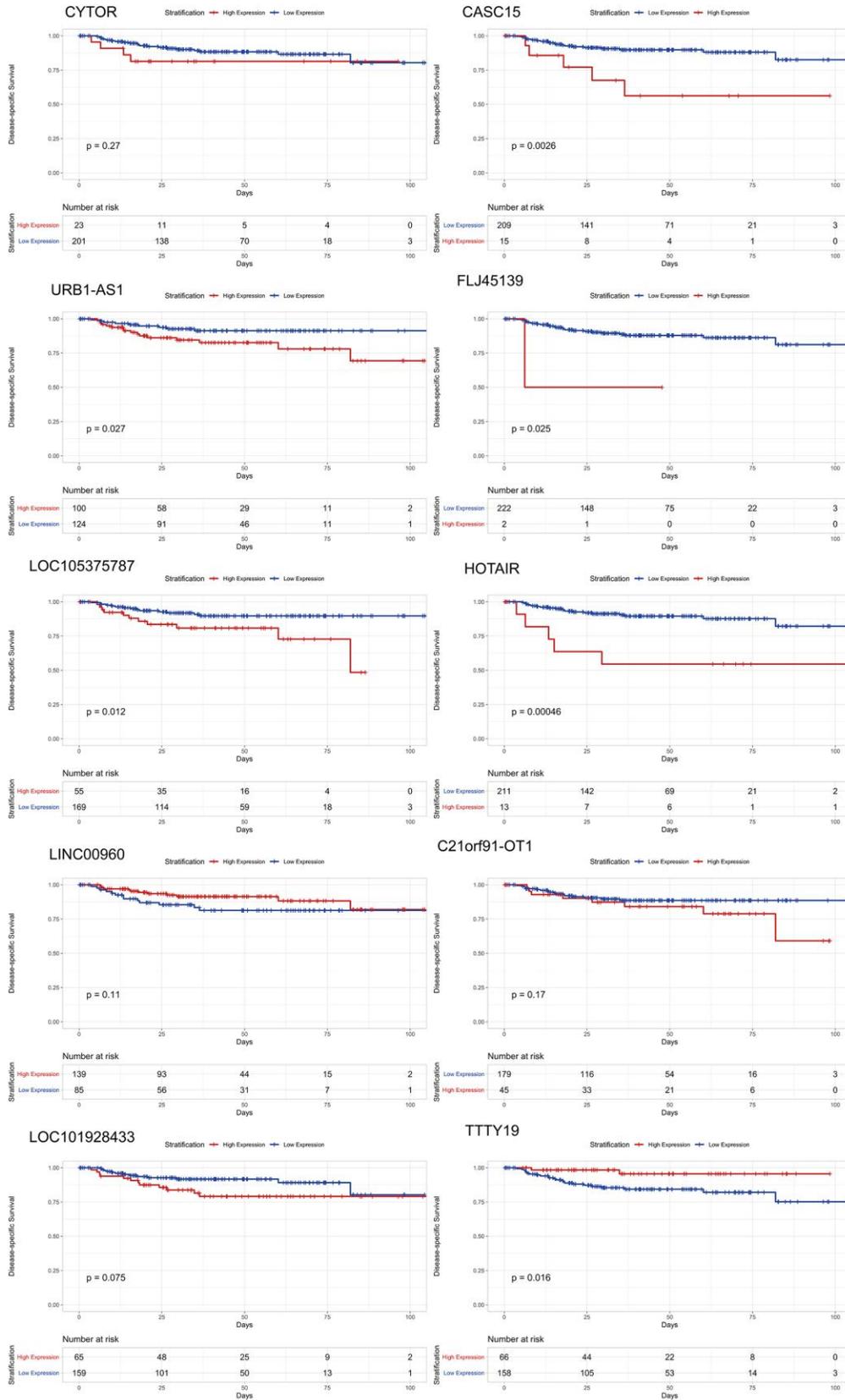


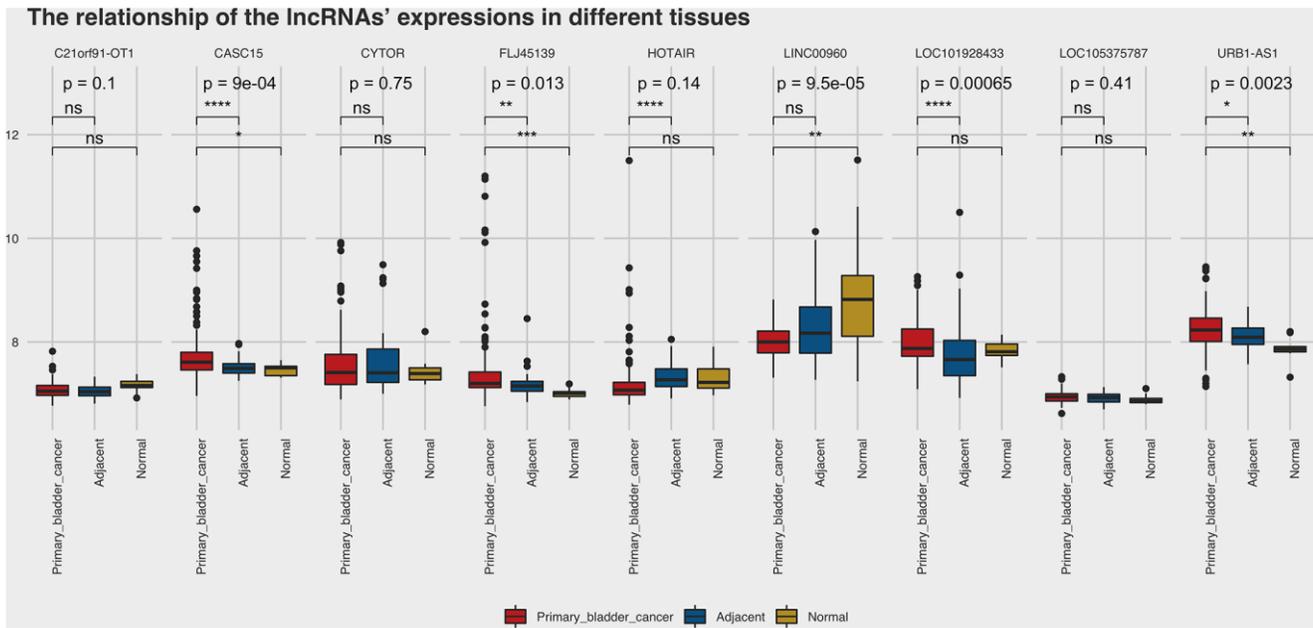
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Visualization of random survival forest-variable hunting analysis for identifying the ten most valuable prognostic lncRNAs.



Supplementary Figure 2. Kaplan-Meier estimates of the patients in GSE32894. According to the ncRNA expression level, the patients were divided into two groups grouped using the k-means clustering algorithm.



Supplementary Figure 3. Comparison of the expression levels of the 9 (9 out of 10) prognostic lncRNAs in BLCA tissue (n=165), cancer-adjacent tissue (n=58) and normal bladder mucosa (n=9) in GSE13507.